



## **RAW SEQUENCE LISTING ERROR REPORT**

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Application Serial Number: 10/015,186  
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Date Processed by STIC: 1/2/2002

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OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/015,186

DATE: 01/02/2002  
TIME: 11:29:35

Input Set : A:\1718-0195P.ST25.txt  
Output Set: N:\CRF3\01022002\J015186.raw

*pp 1,3*

**Does Not Comply  
Corrected Diskette Needed**

*OK*

3 <110> APPLICANT: Quibell, Martin  
4 Taylor, Steven  
5 Grabowska, Urszula  
6 Nilsson, Magnus  
7 Morisson, Veronique  
9 <120> TITLE OF INVENTION: Cysteine Protease Inhibitors  
11 <130> FILE REFERENCE: 1718-0195P  
13 <140> CURRENT APPLICATION NUMBER: US/10/015,186  
13 <141> CURRENT FILING DATE: 2001-11-16  
13 <150> PRIOR APPLICATION NUMBER: US 60/252,840  
14 <151> PRIOR FILING DATE: 2000-11-17  
16 <150> PRIOR APPLICATION NUMBER: PCT/GB00/01894  
17 <151> PRIOR FILING DATE: 2000-05-18  
19 <150> PRIOR APPLICATION NUMBER: GB9911417.5  
20 <151> PRIOR FILING DATE: 1999-05-18  
22 <160> NUMBER OF SEQ ID NOS: 4  
24 <170> SOFTWARE: PatentIn version 3.0  
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v--> 31 <223> OTHER INFORMATION:  
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41 <223> OTHER INFORMATION: Primer for cDNA of cysteinyl proteinase (Falcipain 2)  
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50 <213> ORGANISM: artificial sequence  
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53 <223> OTHER INFORMATION: PCR product from amplification using primers for the cDNA  
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57 <221> NAME/KEY: CDS  
58 <222> LOCATION: (3)..(848)  
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63 1 5 10 15

*see item 11 on Euro Summary Sheet*

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Input Set : A:\1718-0195P.ST25.txt

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67          20          25          30
69 tat tta tta gat caa atg aat tat gaa gaa gtt ata aaa aaa tat aga      143
70 Tyr Leu Leu Asp Gln Met Asn Tyr Glu Glu Val Ile Lys Lys Tyr Arg
71          35          40          45
73 gga gaa gaa aat ttc gat cat gca gct tac gac tgg aga tta cac agt      191
74 Gly Glu Glu Asn Phe Asp His Ala Ala Tyr Asp Trp Arg Leu His Ser
75          50          55          60
77 ggt gta aca cct gta aag gat caa aaa aat tgt gga tct tgc tgg gcc      239
78 Gly Val Thr Pro Val Lys Asp Gln Lys Asn Cys Gly Ser Cys Trp Ala
79          65          70          75
81 ttt agt agt ata ggt tcc gta gaa tca caa tat gct atc aga aaa aat      287
82 Phe Ser Ser Ile Gly Ser Val Glu Ser Gln Tyr Ala Ile Arg Lys Asn
83 80          85          90          95
85 aaa tta ata acc tta agt gaa caa gaa tta gta gat tgt tca ttt aaa      335
86 Lys Leu Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys Ser Phe Lys
87          100          105          110
89 aat tat ggt tgt aat gga ggt ctc att aat aat gcc ttt gag gat atg      383
90 Asn Tyr Gly Cys Asn Gly Gly Leu Ile Asn Asn Ala Phe Glu Asp Met
91          115          120          125
93 att gaa ctt gga ggt ata tgt cca gat ggt gat tat cca tat gtg agt      431
94 Ile Glu Leu Gly Gly Ile Cys Pro Asp Gly Asp Tyr Pro Tyr Val Ser
95          130          135          140
97 gat gct cca aat tta tgt aac ata gat aga tgt act gaa aaa tat gga      479
98 Asp Ala Pro Asn Leu Cys Asn Ile Asp Arg Cys Thr Glu Lys Tyr Gly
99          145          150          155
101 atc aaa aat tat tta tcc gta cca gat aat aaa tta aaa gaa gca ctt      527
102 Ile Lys Asn Tyr Leu Ser Val Pro Asp Asn Lys Leu Lys Glu Ala Leu
103 160          165          170          175
105 aga ttc ttg gga cct att agt att agt gta gcc gta tca gat gat ttt      575
106 Arg Phe Leu Gly Pro Ile Ser Ile Ser Val Ala Val Ser Asp Asp Phe
107          180          185          190
109 gct ttt tac aaa gaa ggt att ttc gat gga gaa tgt ggt gat gaa tta      623
110 Ala Phe Tyr Lys Glu Gly Ile Phe Asp Gly Glu Cys Gly Asp Glu Leu
111          195          200          205
113 aat cat gcc gtt atg ctt gta ggt ttt ggt atg aaa gaa att gtt aat      671
114 Asn His Ala Val Met Leu Val Gly Phe Gly Met Lys Glu Ile Val Asn
115          210          215          220
117 cca tta acc aag aaa gga gaa aaa cat tat tat tat ata att aag aac      719
118 Pro Leu Thr Lys Lys Gly Glu Lys His Tyr Tyr Tyr Ile Ile Lys Asn
119          225          230          235
121 tca tgg gga caa caa tgg gga gaa aga ggt ttc ata aat att gaa aca      767
122 Ser Trp Gly Gln Gln Trp Gly Glu Arg Gly Phe Ile Asn Ile Glu Thr
123 240          245          250          255
125 gat gaa tca gga tta atg aga aaa tgt gga tta ggt act gat gca ttc      815
126 Asp Glu Ser Gly Leu Met Arg Lys Cys Gly Leu Gly Thr Asp Ala Phe
127          260          265          270
129 att cca tta att gaa cat cat cat cat cat cat taagtcgacg cgatcgaatt      868

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130 Ile Pro Leu Ile Glu His His His His His His  
 131 275 280  
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 136 <210> SEQ ID NO: 4  
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 141 <220> FEATURE:  
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 148 20 25 30  
 151 Leu Leu Asp Gln Met Asn Tyr Glu Glu Val Ile Lys Lys Tyr Arg Gly  
 152 35 40 45  
 155 Glu Glu Asn Phe Asp His Ala Ala Tyr Asp Trp Arg Leu His Ser Gly  
 156 50 55 60  
 159 Val Thr Pro Val Lys Asp Gln Lys Asn Cys Gly Ser Cys Trp Ala Phe  
 160 65 70 75 80  
 163 Ser Ser Ile Gly Ser Val Glu Ser Gln Tyr Ala Ile Arg Lys Asn Lys  
 164 85 90 95  
 167 Leu Ile Thr Leu Ser Glu Gln Glu Leu Val Asp Cys Ser Phe Lys Asn  
 168 100 105 110  
 171 Tyr Gly Cys Asn Gly Gly Leu Ile Asn Asn Ala Phe Glu Asp Met Ile  
 172 115 120 125  
 175 Glu Leu Gly Gly Ile Cys Pro Asp Gly Asp Tyr Pro Tyr Val Ser Asp  
 176 130 135 140  
 179 Ala Pro Asn Leu Cys Asn Ile Asp Arg Cys Thr Glu Lys Tyr Gly Ile  
 180 145 150 155 160  
 183 Lys Asn Tyr Leu Ser Val Pro Asp Asn Lys Leu Lys Glu Ala Leu Arg  
 184 165 170 175  
 187 Phe Leu Gly Pro Ile Ser Ile Ser Val Ala Val Ser Asp Asp Phe Ala  
 188 180 185 190  
 191 Phe Tyr Lys Glu Gly Ile Phe Asp Gly Glu Cys Gly Asp Glu Leu Asn  
 192 195 200 205  
 195 His Ala Val Met Leu Val Gly Phe Gly Met Lys Glu Ile Val Asn Pro  
 196 210 215 220  
 199 Leu Thr Lys Lys Gly Glu Lys His Tyr Tyr Tyr Ile Ile Lys Asn Ser  
 200 225 230 235 240  
 203 Trp Gly Gln Gln Trp Gly Glu Arg Gly Phe Ile Asn Ile Glu Thr Asp  
 204 245 250 255  
 207 Glu Ser Gly Leu Met Arg Lys Cys Gly Leu Gly Thr Asp Ala Phe Ile  
 208 260 265 270  
 211 Pro Leu Ile Glu His His His His His His  
 212 275 280

886

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/015,186

DATE: 01/02/2002

TIME: 11:29:36

Input Set : A:\1718-0195P.ST25.txt

Output Set: N:\CRF3\01022002\J015186.raw

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 L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:31 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:31 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
 L:139 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
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